

#2 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,356

DATE: 12/13/2001

TIME: 09:00:36

Input Set : A:\00-107.SEQ.txt

Output Set: N:\CRF3\12132001\I003356.raw

4 <110> APPLICANT: Lok, Si  
5 Holloway, James L.  
7 <120> TITLE OF INVENTION: Human V2 Vomeronasal Receptor  
9 <130> FILE REFERENCE: 00-107  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/003,356  
C--> 11 <141> CURRENT FILING DATE: 2001-11-15  
11 <150> PRIOR APPLICATION NUMBER: 60/252,373  
12 <151> PRIOR FILING DATE: 2000-11-21  
14 <160> NUMBER OF SEQ ID NOS: 10  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 657  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
23 <220> FEATURE:  
24 <221> NAME/KEY: CDS  
25 <222> LOCATION: (1)...(657)  
27 <400> SEQUENCE: 1  
28 atg ttt gag agg cgc aaa gag caa gac gag gga cca gga atc cat gaa 48  
29 Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu  
30 1 5 10 15  
32 ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96  
33 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu  
34 20 25 30  
36 aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144  
37 Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala  
38 35 40 45  
40 gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192  
41 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg  
42 50 55 60  
44 acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt 240  
45 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys  
46 65 70 75 80  
48 gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac 288  
49 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His  
50 85 90 95  
52 atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act 336  
53 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr  
54 100 105 110  
56 ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg 384  
57 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val  
58 115 120 125  
60 gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat 432  
61 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn  
62 130 135 140  
64 ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt 480  
65 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly

ENTERED

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66 145          150          155          160
68 gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat 528
69 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
70          165          170          175
72 ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa 576
73 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
74          180          185          190
76 tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag 624
77 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
78          195          200          205
80 tcg aag gct gtg gta aaa cgt atc caa cac ttt 657
81 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
82 210          215
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 219
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 2
90 Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu
91 1          5          10          15
92 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
93          20          25          30
94 Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
95          35          40          45
96 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
97          50          55          60
98 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
99 65          70          75          80
100 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
101          85          90          95
102 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
103          100          105          110
104 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
105          115          120          125
106 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
107          130          135          140
108 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
109 145          150          155          160
110 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
111          165          170          175
112 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
113          180          185          190
114 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
115          195          200          205
116 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
117          210          215
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 657
121 <212> TYPE: DNA

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122 &lt;213&gt; ORGANISM: Artificial Sequence

124 &lt;220&gt; FEATURE:

125 <223> OTHER INFORMATION: This degenerate nucleotide sequence encodes the  
126 amino acid sequence of SEQ ID NO:2.

128 &lt;221&gt; NAME/KEY: misc\_feature

129 &lt;222&gt; LOCATION: 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111,

130 114, 120, 123, 126, 129, 138, 144, 156, 159, 162, 168, 171,

131 174, 180, 189, 192, 195, 201, 204, 213, 219, 225, 228, 231,

132 234, 246, 261, 267, 279, 312, 324, 327, 336, 339, 342

133 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

135 &lt;221&gt; NAME/KEY: misc\_feature

136 &lt;222&gt; LOCATION: 360, 369, 375, 381, 384, 390, 393, 396, 399, 405, 408, 411,

137 426, 429, 438, 444, 447, 450, 453, 459, 462, 465, 471, 474,

138 477, 480, 483, 486, 492, 495, 498, 501, 504, 507, 510, 516,

139 519, 522, 531, 534, 540, 543, 549, 552, 555, 561, 567

140 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

142 &lt;221&gt; NAME/KEY: misc\_feature

143 &lt;222&gt; LOCATION: 570, 588, 591, 597, 600, 603, 609, 612, 627, 633, 636, 639,

144 645

145 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

147 &lt;400&gt; SEQUENCE: 3

W--&gt; 148 atgttygarm gnmгнаarga rcargaygar ggnccnggna thcaygartt yytngcntty 60

W--&gt; 149 ytntggcng arytnngnws ngargcnaar gargaraarg argargarmg nactngymgn 120

W--&gt; 150 ytnytnggna artgygtnga ygcngaraay caywsnytng tnathggngg nytnttyccn 180

W--&gt; 151 athgaywsnm gnacnathcc ngcnaaygar wsnathytng arccngcnws ngcnaartgy 240

W--&gt; 152 gargnttya ayttycarmg nttymgntgg atgaargcna tgathcayat gathaargar 300

W--&gt; 153 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayacn 360

W--&gt; 154 tgyttyacna thwsnaarws ngtnargcn gtnytngnt tyytnacngg ncargargar 420

W--&gt; 155 aaymgncna ayttymgnaa ywsnacnggn gcnttyccng cnggnathgt ngngcnggn 480

W--&gt; 156 ggnwsnttyy tnwsngtncc ngcnwsnmgn athytnggny tntaytayt nccncargtn 540

W--&gt; 157 ggntayacnw snactgygt nathytnwsn gayaartayc arttyccnws ntayytngmgn 600

W--&gt; 158 gtnathgcnw sngayaarat hcarwsnaar gcngtngtna armgnathca rcaytty 657

160 &lt;210&gt; SEQ ID NO: 4

161 &lt;211&gt; LENGTH: 1140

162 &lt;212&gt; TYPE: DNA

163 &lt;213&gt; ORGANISM: Homo sapiens

165 &lt;220&gt; FEATURE:

166 &lt;221&gt; NAME/KEY: CDS

167 &lt;222&gt; LOCATION: (1)...(1140)

169 &lt;400&gt; SEQUENCE: 4

170 ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg act gga agg 48

171 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg

172 1 5 10 15

174 gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt 96

175 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys

176 20 25 30

178 gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa 144

179 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln

180 35 40 45

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182	tgt	ggt	gaa	gac	tat	tgg	tca	aat	gca	caa	aag	agc	gag	tgt	gtg	ctg	192
183	Cys	Gly	Glu	Asp	Tyr	Trp	Ser	Asn	Ala	Gln	Lys	Ser	Glu	Cys	Val	Leu	
184		50					55				60						
186	aaa	gag	gtg	gaa	tac	ctt	gct	tat	gat	gag	gcc	ctg	gga	ttc	aca	ctt	240
187	Lys	Glu	Val	Glu	Tyr	Leu	Ala	Tyr	Asp	Glu	Ala	Leu	Gly	Phe	Thr	Leu	
188	65					70					75					80	
190	gtc	att	ctt	tct	gtc	ttt	ggg	gca	ttt	gtg	gtc	ttg	gca	gtc	aca	gct	288
191	Val	Ile	Leu	Ser	Val	Phe	Gly	Ala	Phe	Val	Val	Leu	Ala	Val	Thr	Ala	
192					85					90					95		
194	gtg	tat	gtg	ata	cac	agg	cac	act	ccc	ctg	gtg	aac	gcc	agt	gac	tgg	336
195	Val	Tyr	Val	Ile	His	Arg	His	Thr	Pro	Leu	Val	Asn	Ala	Ser	Asp	Trp	
196				100					105					110			
198	cag	ctg	ggc	ttt	ctc	att	cag	gtt	tct	ctg	atc	atc	atg	ctg	ctg	tcg	384
199	Gln	Leu	Gly	Phe	Leu	Ile	Gln	Val	Ser	Leu	Ile	Ile	Met	Leu	Leu	Ser	
200			115					120					125				
202	tcc	atg	ctt	ttc	att	gac	aag	cca	cac	aac	tgg	tcc	tgc	atg	gct	ggc	432
203	Ser	Met	Leu	Phe	Ile	Asp	Lys	Pro	His	Asn	Trp	Ser	Cys	Met	Ala	Gly	
204		130					135					140					
206	cag	gtc	act	ctg	gca	ctg	ggc	ttt	tct	ctt	tgc	ctg	tct	tgc	ctt	ctt	480
207	Gln	Val	Thr	Leu	Ala	Leu	Gly	Phe	Ser	Leu	Cys	Leu	Ser	Cys	Leu	Leu	
208	145					150					155					160	
210	gga	aag	act	agt	tca	ctg	ttt	tta	gcc	tac	aga	att	tcc	aaa	tcc	aaa	528
211	Gly	Lys	Thr	Ser	Ser	Leu	Phe	Leu	Ala	Tyr	Arg	Ile	Ser	Lys	Ser	Lys	
212				165						170				175			
214	act	caa	ctt	aca	tcc	atg	cac	ccc	ctt	tat	cgg	aaa	atc	att	gtg	cta	576
217	Thr	Gln	Leu	Thr	Ser	Met	His	Pro	Leu	Tyr	Arg	Lys	Ile	Ile	Val	Leu	
218				180					185					190			
220	atc	tct	gtt	cta	gcg	gag	att	ggc	ata	tgt	aca	gcc	tac	ttg	ata	ttg	624
221	Ile	Ser	Val	Leu	Ala	Glu	Ile	Gly	Ile	Cys	Thr	Ala	Tyr	Leu	Ile	Leu	
222			195					200					205				
224	gaa	cct	ccc	atg	gta	tac	aag	aac	atg	gaa	tct	caa	aat	aca	aag	atc	672
225	Glu	Pro	Pro	Met	Val	Tyr	Lys	Asn	Met	Glu	Ser	Gln	Asn	Thr	Lys	Ile	
226		210					215					220					
228	att	ctg	gga	tgc	aat	gaa	att	tcc	ata	gag	ttt	ttg	tac	tcg	atg	ttt	720
229	Ile	Leu	Gly	Cys	Asn	Glu	Ile	Ser	Ile	Glu	Phe	Leu	Tyr	Ser	Met	Phe	
230	225					230					235					240	
232	gga	att	gat	gcc	ttc	tta	gcc	ttg	cta	tgc	ttt	ctt	aca	act	ttt	gtg	768
233	Gly	Ile	Asp	Ala	Phe	Leu	Ala	Leu	Leu	Cys	Phe	Leu	Thr	Thr	Phe	Val	
234				245						250					255		
236	gct	cgc	cag	tta	cca	gat	aat	tac	tat	gaa	gga	aaa	tgc	atc	acc	ttt	816
237	Ala	Arg	Gln	Leu	Pro	Asp	Asn	Tyr	Tyr	Glu	Gly	Lys	Cys	Ile	Thr	Phe	
238				260					265					270			
240	ggg	atg	ctt	gtc	ttt	ttc	atc	att	tgg	atg	tct	ttt	gtc	cct	gtt	tat	864
241	Gly	Met	Leu	Val	Phe	Phe	Ile	Ile	Trp	Met	Ser	Phe	Val	Pro	Val	Tyr	
242			275					280					285				
244	ttg	agc	acc	aaa	ggc	aag	ttc	aaa	atg	gct	gtg	gaa	ata	ttt	gca	atc	912
245	Leu	Ser	Thr	Lys	Gly	Lys	Phe	Lys	Met	Ala	Val	Glu	Ile	Phe	Ala	Ile	
246		290					295					300					
248	ttg	gca	tcc	agc	cat	ggc	ttg	ttg	ggt	tgt	ata	ttt	gct	cct	aag	tgc	960

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```

249 Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys
250 305          310          315          320
252 ctc att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt 1008
253 Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys
254          325          330          335
256 gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc tca gct ttt 1056
257 Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe
258          340          345          350
260 gtg agc agt gag ctt aac aat acc aca gtg tca act gtt ctg gat gac 1104
261 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
262          355          360          365
264 aga gtt ttg att tac atg tgt cct ttg aag ctg caa 1140
265 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
266          370          375          380
268 <210> SEQ ID NO: 5
269 <211> LENGTH: 380
270 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
273 <400> SEQUENCE: 5
274 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg
275 1          5          10          15
276 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys
277          20          25          30
278 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln
279          35          40          45
280 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu
281          50          55          60
282 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu
283 65          70          75          80
284 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala
285          85          90          95
286 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp
287          100         105         110
288 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser
289          115         120         125
290 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly
291          130         135         140
292 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu
293 145         150         155         160
294 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys
295          165         170         175
296 Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu
297          180         185         190
298 Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu
299          195         200         205
300 Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile
301          210         215         220
302 Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe
303 225         230         235         240

```

→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.



## VERIFICATION SUMMARY

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Input Set : A:\00-107.SEQ.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9